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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/710,058	11/10/2000	David Anderson	A-68531-1/RMS/JJD/SPL	4112

7590 02/27/2002

Flehr Hohbach Test Albritton & Herbert LLP
Suite 3400
Four Embarcadero Center
San Francisco, CA 94111-4187

EXAMINER

CELSA, BENNETT M

ART UNIT PAPER NUMBER

1627

DATE MAILED: 02/27/2002

Please find below and/or attached an Office communication concerning this application or proceeding.

file
copy



UNITED STATES DEPARTMENT OF COMMERCE
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SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.
09/710,058			

EXAMINER	
ART UNIT	PAPER NUMBER
1627	5

Please find below a communication from the EXAMINER in charge of this application

Sequence Rule Compliance: Bonafide Attempt Letter

Applicant's computer readable form (CRF) has been received. However, this application fails to comply with the requirements of 37 C.F.R. §§ 1.821-1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures and **RAW SEQUENCE LISTING ERROR REPORT**.

APPLICANT IS GIVEN 30 days FROM THE DATE OF THIS LETTER WITHIN WHICH TO COMPLY WITH THE SEQUENCE RULES, 37 C.R.F. §§ 1.821-1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 C.F.R. § 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 C.F.R. § 1.136. In no case may an applicant extend the period for response beyond the six month statutory period. Direct the response to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the response.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Examiner Celsa whose telephone number is (703) 305-7556. If the examiner cannot be reached, inquiries can be directed to Supervisory Patent Examiner Venkat whose telephone number is (703) 308-0570. The fax number for the organization where this application or proceeding is assigned is (703) 308-4242. Any inquiry of a general nature or relating to the status of this application should be directed to the Group receptionist whose telephone number is (703) 308-0196.

Bennett Celsa (au 1627) (Feb. 25, 2002)

BENNETT CELSA
PRIMARY EXAMINER

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 CFR 1.821 - 1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821.
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached marked-up copy of the "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).
- ☒ 7. Other: SEE ATTACHED CRF ERROR REPORT

Applicant must provide:

- ☒ An ~~initial~~ or substitute computer readable form (CRF) copy of the "Sequence Listing"
- ☒ An ~~initial~~ or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact:

For Rules Interpretation, call (703) 308-1123
 For CRF submission help, call (703) 308-4212
 For PatentIn software help, call (703) 308-6856

Please return a copy of this notice with your response.

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/7/0,058

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) **(2) INFORMATION FOR SEQ ID NO:X:**
 (i) **SEQUENCE CHARACTERISTICS:**(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (xi) **SEQUENCE DESCRIPTION:SEQ ID NO:X:**
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) **<210> sequence id number**
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
- 11 Use of "Artificial" Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
(NEW RULES) Valid response is Artificial Sequence.
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
 Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" **Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1646

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/710,058

DATE: 04/24/2001

TIME: 13:20:15

Input Set : A:\A68531-1.ST25.txt

Output Set: N:\CRF3\04242001\I710058.raw

Does Not Comply
Corrected Diskette Needed
see p. 6

```

3 <110> APPLICANT: Anderson, David
5 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS COMPRISING RENILLA GFP
7 <130> FILE REFERENCE: A-68531-1/DJB/RMS/AMS
9 <140> CURRENT APPLICATION NUMBER: US 09/710,058
10 <141> CURRENT FILING DATE: 2000-11-10
12 <150> PRIOR APPLICATION NUMBER: US 60/164,592
13 <151> PRIOR FILING DATE: 1999-11-10.
15 <160> NUMBER OF SEQ ID NOS: 85
17 <170> SOFTWARE: PatentIn version 3.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1079
21 <212> TYPE: DNA
22 <213> ORGANISM: Renilla muelleri
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (259)..(975)
28 <400> SEQUENCE: 1
29 ggttatacac aagtgtatcg cgtatctgca gacgcatcta gtgggattat tcgagcggta      60
31 gtatttacgt cagacctgtc taatcgaaac cacaacaaac tcttaaaata agccacattt      120
33 acataatata taagagacgc ctcatTTaag agtagtaaaa atataatata tgatagagta      180
35 tacaactctc gccttagaca gacagtgtgc aacagagtaa ctcttgTTaa tgcaatcgaa      240
37 agcgtcaaga gagataag atg agt aaa caa ata ttg aag aac act tgt tta      291
38                               Met Ser Lys Gln Ile Leu Lys Asn Thr Cys Leu
39                               1               5               10
41 caa gaa gta atg tcg tat aaa gta aat ctg gaa gga att gta aac aac      339
42 Gln Glu Val Met Ser Tyr Lys Val Asn Leu Glu Gly Ile Val Asn Asn
43                               15               20               25
45 cat gtt ttt aca atg gag ggt tgc ggc aaa ggg aat att tta ttc ggc      387
46 His Val Phe Thr Met Glu Gly Cys Gly Lys Gly Asn Ile Leu Phe Gly
47                               30               35               40
49 aat caa ctg gtt cag att cgt gtc acg aaa ggg gcc cca ctg cct ttt      435
50 Asn Gln Leu Val Gln Ile Arg Val Thr Lys Gly Ala Pro Leu Pro Phe
51                               45               50               55
53 gca ttt gat att gtg tca cca gct ttt caa tat ggc aac cgt act ttc      483
54 Ala Phe Asp Ile Val Ser Pro Ala Phe Gln Tyr Gly Asn Arg Thr Phe
55 60                               65               70               75
57 acg aaa tat ccg aat gat ata tca gat tat ttt ata caa tca ttt cca      531
58 Thr Lys Tyr Pro Asn Asp Ile Ser Asp Tyr Phe Ile Gln Ser Phe Pro
59                               80               85               90
61 gca gga ttt atg tat gaa cga aca tta cgt tac gaa gat ggc gga ctt      579
62 Ala Gly Phe Met Tyr Glu Arg Thr Leu Arg Tyr Glu Asp Gly Gly Leu
63                               95               100              105
65 gtt gaa att cgt tca gat ata aat tta ata gaa gac aag ttc gtc tac      627
66 Val Glu Ile Arg Ser Asp Ile Asn Leu Ile Glu Asp Lys Phe Val Tyr
67                               110              115              120
69 aga gtc gaa tac aaa ggt agt aac ttc cca gat gat ggt ccc gtc atg      675
70 Arg Val Glu Tyr Lys Gly Ser Asn Phe Pro Asp Asp Gly Pro Val Met

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/710,058

DATE: 04/24/2001

TIME: 13:20:15

Input Set : A:\A68531-1.ST25.txt

Output Set: N:\CRF3\04242001\I710058.raw

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71      125      130      135
73 cag aag act atc tta gga ata gag cct tca ttt gaa gcc atg tac atg      723
74 Gln Lys Thr Ile Leu Gly Ile Glu Pro Ser Phe Glu Ala Met Tyr Met
75 140      145      150      155
77 aat aat ggc gtc ttg gtc ggc gaa gta att ctt gtc tat aaa cta aac      771
78 Asn Asn Gly Val Leu Val Gly Glu Val Ile Leu Val Tyr Lys Leu Asn
79      160      165      170
81 tct ggg aaa tat tat tca tgt cac atg aaa aca tta atg aag tcg aaa      819
82 Ser Gly Lys Tyr Tyr Ser Cys His Met Lys Thr Leu Met Lys Ser Lys
83      175      180      185
85 ggt gta gta aag gag ttt cct tcg tat cat ttt att caa cat cgt ttg      867
86 Gly Val Val Lys Glu Phe Pro Ser Tyr His Phe Ile Gln His Arg Leu
87      190      195      200
89 gaa aag act tac gta gaa gac ggg ggg ttc gtt gaa cag cat gag act      915
90 Glu Lys Thr Tyr Val Glu Asp Gly Gly Phe Val Glu Gln His Glu Thr
91      205      210      215
93 gct att gct caa atg aca tct ata gga aaa cca cta gga tcc tta cac      963
94 Ala Ile Ala Gln Met Thr Ser Ile Gly Lys Pro Leu Gly Ser Leu His
95 220      225      230      235
97 gaa tgg gtt taa acacagttac attacttttt ccaattcgtg tttcatgtca      1015
98 Glu Trp Val
101 aataataatt ttttaaacaa ttatcaatgt tttgtgatat gtttgtaaaa aaaaaaaaaa      1075
103 aaaa      1079
106 <210> SEQ ID NO: 2
107 <211> LENGTH: 238
108 <212> TYPE: PRT
109 <213> ORGANISM: Renilla muelleri
111 <400> SEQUENCE: 2
113 Met Ser Lys Gln Ile Leu Lys Asn Thr Cys Leu Gln Glu Val Met Ser
114 1      5      10      15
117 Tyr Lys Val Asn Leu Glu Gly Ile Val Asn Asn His Val Phe Thr Met
118      20      25      30
121 Glu Gly Cys Gly Lys Gly Asn Ile Leu Phe Gly Asn Gln Leu Val Gln
122      35      40      45
125 Ile Arg Val Thr Lys Gly Ala Pro Leu Pro Phe Ala Phe Asp Ile Val
126      50      55      60
129 Ser Pro Ala Phe Gln Tyr Gly Asn Arg Thr Phe Thr Lys Tyr Pro Asn
130 65      70      75      80
133 Asp Ile Ser Asp Tyr Phe Ile Gln Ser Phe Pro Ala Gly Phe Met Tyr
134      85      90      95
137 Glu Arg Thr Leu Arg Tyr Glu Asp Gly Gly Leu Val Glu Ile Arg Ser
138      100      105      110
141 Asp Ile Asn Leu Ile Glu Asp Lys Phe Val Tyr Arg Val Glu Tyr Lys
142      115      120      125
145 Gly Ser Asn Phe Pro Asp Asp Gly Pro Val Met Gln Lys Thr Ile Leu
146      130      135      140
149 Gly Ile Glu Pro Ser Phe Glu Ala Met Tyr Met Asn Asn Gly Val Leu
150 145      150      155      160
153 Val Gly Glu Val Ile Leu Val Tyr Lys Leu Asn Ser Gly Lys Tyr Tyr

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RAW SEQUENCE LISTING

DATE: 04/24/2001

PATENT APPLICATION: US/09/710,058

TIME: 13:20:15

Input Set : A:\A68531-1.ST25.txt

Output Set: N:\CRF3\04242001\I710058.raw

```

154                               165                               170                               175
157 Ser Cys His Met Lys Thr Leu Met Lys Ser Lys Gly Val Val Lys Glu
158                               180                               185                               190
161 Phe Pro Ser Tyr His Phe Ile Gln His Arg Leu Glu Lys Thr Tyr Val
162                               195                               200                               205
165 Glu Asp Gly Gly Phe Val Glu Gln His Glu Thr Ala Ile Ala Gln Met
166                               210                               215                               220
169 Thr Ser Ile Gly Lys Pro Leu Gly Ser Leu His Glu Trp Val
170 225                               230                               235
173 <210> SEQ ID NO: 3
174 <211> LENGTH: 1104
175 <212> TYPE: DNA
176 <213> ORGANISM: Ptilosarcus Gurneyi
178 <400> SEQUENCE: 3
179 tcggcacgag ctggcctcca cactttagac aaaatgaacc gcaacgtatt aaagaacact      60
181 ggactgaaag agattatgtc ggcaaaagct agcgttgaag gaatcgtgaa caatcacggt      120
183 ttttccatgg aaggatttgg aaaaggcaat gtattatttg gaaaccaatt gatgcaaadc      180
185 cgggttacaa agggaggtcc gttgccattc gctttcgata ttgtttccat agctttccaa      240
187 tacgggaatc gcactttcac gaaataccca gacgacattg cggactactt tgttcaatca      300
189 ttcccggtcg gattttttcta cgaaagaaat ctacgctttg aagatggcgc cattgttgac      360
191 attcgttcag atataagttt agaagatgat aagttccact acaaagtgga gtatagaggc      420
193 aacggtttcc ctagtaacgg acccgtgatg caaaaagcca tcctcggcat ggagccatcg      480
195 tttgaggtgg tctacatgaa cagcggcggt ctggtgggcg aagtagatct cgtttacaaa      540
197 ctcgagtcag ggaactatta ctctgcccac atgaaaacgt tttacagatc caaaggtgga      600
199 gtgaaagaat tcccggaata tcactttatc catcatcgtc tggagaaaac ctacgtggaa      660
201 gaaggaagct tcgtggaaca acacgagacg gccattgcac aactgaccac aattggaaaa      720
203 cctctgggct cccttcatga atgggtgtag aaaatgacca atatactggg gaaaccgata      780
205 accgtttgga agcttgtgta tacaattat ttggggtcat tttgtaatgt gtatgtgtgt      840
207 tgtatgatca atagacgtcg tcattcatag cttgaatcct tcagcaaaaag aaacctcgaa      900
209 gcatattgaa acctcgaagc atattgaaac ctcgacggag agcgtaaaga gaccgcacaa      960
211 attaacgcgt ttcaaccagc agttggaatc tttaaaccga tcaaaactat taatataaat      1020
213 atatatacc tgtataactt atatatatct atatagtttg atattgatta aatctgttct      1080
215 tgatcaaaaa aaaaaaaaaa aaaa
218 <210> SEQ ID NO: 4
219 <211> LENGTH: 1279
220 <212> TYPE: DNA
221 <213> ORGANISM: Ptilosarcus Gurneyi
223 <220> FEATURE:
224 <221> NAME/KEY: CDS
225 <222> LOCATION: (7)..(720)
227 <400> SEQUENCE: 4
228 gacaaa atg aac cgc aac gta tta aag aac act gga ctg aaa gag att      48
229 Met Asn Arg Asn Val Leu Lys Asn Thr Gly Leu Lys Glu Ile
230 1 5 10
232 atg tcg gca aaa gct agc gtt gaa gga atc gtg aac aat cac gtt ttt      96
233 Met Ser Ala Lys Ala Ser Val Glu Gly Ile Val Asn Asn His Val Phe
234 15 20 25 30
236 tcc atg gaa gga ttt gga aaa ggc aat gta tta ttt gga aac caa ttg      144
237 Ser Met Glu Gly Phe Gly Lys Gly Asn Val Leu Phe Gly Asn Gln Leu

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RAW SEQUENCE LISTING

DATE: 04/24/2001

PATENT APPLICATION: US/09/710,058

TIME: 13:20:15

Input Set : A:\A68531-1.ST25.txt

Output Set: N:\CRF3\04242001\I710058.raw

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238          35          40          45
240 atg caa atc cgg gtt aca aag gga ggt ccg ttg cca ttc gct ttc gac      192
241 Met Gln Ile Arg Val Thr Lys Gly Gly Pro Leu Pro Phe Ala Phe Asp
242          50          55          60
244 att gtt tcc ata gct ttc caa tac ggg aat cgc act ttc acg aaa tac      240
245 Ile Val Ser Ile Ala Phe Gln Tyr Gly Asn Arg Thr Phe Thr Lys Tyr
246          65          70          75
248 cca gac gac att gcg gac tac ttt gtt caa tca ttt ccg gct gga ttt      288
249 Pro Asp Asp Ile Ala Asp Tyr Phe Val Gln Ser Phe Pro Ala Gly Phe
250          80          85          90
252 ttc tac gaa aga aat cta cgc ttt gaa gat ggc gcc att gtt gac att      336
253 Phe Tyr Glu Arg Asn Leu Arg Phe Glu Asp Gly Ala Ile Val Asp Ile
254 95          100          105          110
256 cgt tca gat ata agt tta gaa gat gat aag ttc cac tac aaa gtg gag      384
257 Arg Ser Asp Ile Ser Leu Glu Asp Asp Lys Phe His Tyr Lys Val Glu
258          115          120          125
260 tat aga ggc aac ggt ttc cct agt aac gga ccc gtg atg caa aaa gcc      432
261 Tyr Arg Gly Asn Gly Phe Pro Ser Asn Gly Pro Val Met Gln Lys Ala
262          130          135          140
264 atc ctc ggc atg gag cca tcg ttt gag gtg gtc tac atg aac agc ggc      480
265 Ile Leu Gly Met Glu Pro Ser Phe Glu Val Val Tyr Met Asn Ser Gly
266          145          150          155
268 gtt ctg gtg ggc gaa gta gat ctc gtt tac aaa ctc gag tca ggg aac      528
269 Val Leu Val Gly Glu Val Asp Leu Val Tyr Lys Leu Glu Ser Gly Asn
270          160          165          170
272 tat tac tcg tgc cac atg aaa acg ttt tac aga tcc aaa ggt gga gtg      576
273 Tyr Tyr Ser Cys His Met Lys Thr Phe Tyr Arg Ser Lys Gly Gly Val
274 175          180          185          190
276 aaa gaa ttc ccg gaa tat cac ttt atc cat cat cgt ctg gag aaa acc      624
277 Lys Glu Phe Pro Glu Tyr His Phe Ile His His Arg Leu Glu Lys Thr
278          195          200          205
280 tac gtg gaa gaa gga agc ttc gtg gaa caa cac gag acg gcc att gca      672
281 Tyr Val Glu Glu Gly Ser Phe Val Glu Gln His Glu Thr Ala Ile Ala
282          210          215          220
284 caa ctg acc aca att gga aaa cct ctg ggc tcc ctt cat gaa tgg gtg      720
285 Gln Leu Thr Thr Ile Gly Lys Pro Leu Gly Ser Leu His Glu Trp Val
286          225          230          235
288 tagaaaatga ccaatatact ggggaaaatc accaatatac tggggaaaat gaccaattta      780
290 ctggggaaaa tgaccaatat actgtagaaa atcaccaata tactggggaa aatgaccaat      840
292 ttactgggga aatgaccaat ttactgtaga aaatcaccaa tatactgtgg aaaatgacca      900
294 aaatactgta gaaatgttca cactgggttg ataaccgttt cgataaccgt ttggaagctt      960
296 gtgtatacaa gttatttggg gtcattttgt aatgtgtatg tgtgttgtat gatctataga      1020
298 cgtcgtcatt catagcttga atccttcagc aaaagaaacc tcgaagcata ttgaaacctc      1080
300 gacggagagc ataaagagac cgcacgtaca caaattataa taccagcagt tggaatcttt      1140
302 aaaccgatca aaactattaa tatatatata caccctgtat aacatatata tatatatata      1200
304 tctacatagt ttgatattga ttaaattctgt tcttgatcac taiaaaaaaaaa aaaaaaaaaa      1260
306 aaaaaaaaaa aaaaaaaaaa
309 <210> SEQ ID NO: 5
310 <211> LENGTH: 238

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/710,058

DATE: 04/24/2001

TIME: 13:20:15

Input Set : A:\A68531-1.ST25.txt

Output Set: N:\CRF3\04242001\I710058.raw

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311 <212> TYPE: PRT
312 <213> ORGANISM: Ptilosarcus Gurneyi
314 <400> SEQUENCE: 5
316 Met Asn Arg Asn Val Leu Lys Asn Thr Gly Leu Lys Glu Ile Met Ser
317 1 5 10 15
320 Ala Lys Ala Ser Val Glu Gly Ile Val Asn Asn His Val Phe Ser Met
321 20 25 30
324 Glu Gly Phe Gly Lys Gly Asn Val Leu Phe Gly Asn Gln Leu Met Gln
325 35 40 45
328 Ile Arg Val Thr Lys Gly Gly Pro Leu Pro Phe Ala Phe Asp Ile Val
329 50 55 60
332 Ser Ile Ala Phe Gln Tyr Gly Asn Arg Thr Phe Thr Lys Tyr Pro Asp
333 65 70 75 80
336 Asp Ile Ala Asp Tyr Phe Val Gln Ser Phe Pro Ala Gly Phe Phe Tyr
337 85 90 95
340 Glu Arg Asn Leu Arg Phe Glu Asp Gly Ala Ile Val Asp Ile Arg Ser
341 100 105 110
344 Asp Ile Ser Leu Glu Asp Asp Lys Phe His Tyr Lys Val Glu Tyr Arg
345 115 120 125
348 Gly Asn Gly Phe Pro Ser Asn Gly Pro Val Met Gln Lys Ala Ile Leu
349 130 135 140
352 Gly Met Glu Pro Ser Phe Glu Val Val Tyr Met Asn Ser Gly Val Leu
353 145 150 155 160
356 Val Gly Glu Val Asp Leu Val Tyr Lys Leu Glu Ser Gly Asn Tyr Tyr
357 165 170 175
360 Ser Cys His Met Lys Thr Phe Tyr Arg Ser Lys Gly Gly Val Lys Glu
361 180 185 190
364 Phe Pro Glu Tyr His Phe Ile His His Arg Leu Glu Lys Thr Tyr Val
365 195 200 205
368 Glu Glu Gly Ser Phe Val Glu Gln His Glu Thr Ala Ile Ala Gln Leu
369 210 215 220
372 Thr Thr Ile Gly Lys Pro Leu Gly Ser Leu His Glu Trp Val
373 225 230 235
376 <210> SEQ ID NO: 6
377 <211> LENGTH: 238
378 <212> TYPE: PRT
379 <213> ORGANISM: Aequorea victoria
381 <400> SEQUENCE: 6
383 Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
384 1 5 10 15
386 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
387 20 25 30
389 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
390 35 40 45
392 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
393 50 55 60
395 Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
396 65 70 75 80
398 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg

```

009/710,058

6

<210> 8
<211> 244
<212> PRT
<213> Artificial

see item 11 on Error Summary Sheet

(sample of global error)

FYI

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

FYI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/710,058

DATE: 04/24/2001

TIME: 13:20:16

Input Set : A:\A68531-1.ST25.txt

Output Set: N:\CRF3\04242001\I710058.raw

L:483 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
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L:1312 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1315 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
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L:1327 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
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L:1333 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1336 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
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L:1419 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:1425 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/710,058

DATE: 04/24/2001

TIME: 13:20:16

Input Set : A:\A68531-1.ST25.txt

Output Set: N:\CRF3\04242001\I710058.raw

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L:2292 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:78
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